IN THE CLAIMS:

1. (Original) A protein structure comprising a plurality of first peptide monomer units arranged in a first strand and a plurality of second peptide monomer units arranged in a second strand wherein the first and second monomer units comprise the heptad repeat motif (abcdefg) and/or the hendecad repeat motif (abcdefghijk), and wherein a pair of asparagines, arginines, lysines or other complementary residues in the "a" position on at least one pair of corresponding first and second monomer units ensures that the first strand and the second strand form a staggered parallel heterodimer coiled coil structure.

2. (Original) A protein structure according to claim 1, wherein a first peptide monomer unit m the first strand extends beyond a corresponding second peptide monomer unit in the second strand in the direction of the strands.

3. (Original) A protein structure according to anyone of claims 1 to 2 in which at least one charged amino acid residue of a first peptide monomer unit is arranged to attract an oppositely-charged amino acid residue of a second peptide monomer unit.

4. (Original) A protein structure according to claim 3 in which the charged amino acid residue is in an end portion of the first peptide monomer unit which extends beyond the corresponding second peptide monomer unit in the second strand.

5. (Original) A protein structure according to anyone of the preceding claims in which at least one strand consists solely of first or second peptide monomer units respectively.

6. (Original) A protein structure according to anyone of the preceding claims wherein one or more of the other "a" positions of the first and second monomer units is a hydrophobic residue.

7. (Original) A protein structure according to claim 6, wherein the hydrophobic residue is selected from isoleucine or valine.

8. (Original) A protein structure according to anyone of the preceding claims having a leucine at one or more of the "d" positions of the first and second monomer units.

9. (Currently amended) A protein structure according to any one of the preceding claims having oppositely-charged or otherwise complementary residues at positions "g" and "e" of respective monomer units.

10. (Original) A protein structure according to claim 9 in which the opposite-charged residues are glutamic acid and lysine residues or arginine and aspartic acid residues. or synthetic derivatives of these amino acid residues.

11. (Original) A protein structure according to any preceding claim in which the structure is stabilised by pairs of asparagine, arginine, lysine or other complementary residues provided by corresponding first and second peptide monomer units.

12. (Original) A protein structure according to any preceding claim which is arranged to form a tubular structure.

13. (Original) A protein structure according to claim 12 in which the repeat motifs are offset by two or more amino acid positions in sequence whereby the peptide monomer units form a cylinder.

14. (Previously presented) A protein structure according to any preceding claim in which the first and second peptide monomer units have the sequence:

a) KIAALKQKIASLKQEIDALEYENDALEQ (SAF-pl; SEQ ID NO: 1) and

b) KIRALKAKNAHLKQEIAALEQEIAALEQ (SAF-p2; SEQ ID NO: 2) respectively; or

c) KIAALKQKIAALKQEIDALEYENDALEQ (SAF-plA; SEQ ID NO: 3) and

d) KIRALKWKNAHLKQEIAALEQEIAALEQ (SAF-p2C; SEQ ID NO: 4) respectively; or

e) KIAALKQKIASLKQEIDALEYENDALEQ (SAF-p1C; SEQ ID NO: 1) and

f) KIRALKWKNAHLKQEIAALEQEIAALEQ (SAF-p2C; SEQ ID NO: 4) respectively.

15. (Previously presented) A peptide monomer unit for use in preparing a protein structure the peptide monomer unit having an amino acid sequence selected from:

a) KIAALKQKIASLKQEIDALEYENDALEQ (SAF-pl; SEQ ID NO: 1);

b) KIRALKAKNAHLKQEIAALEQEIAALEQ (SAF-p2; SEQ ID NO: 2);

c) KIAALKQKIAALKQEIDALEYENDALEQ (SAF-p1A; SEQ ID NO: 3);

d) KIRALKWKNAHLKQEIAALEQEIAALEQ (SAF-p2C; SEQ ID NO: 5);

e) KIAALKQKIASLKQEIDALEYENDALEQ (SAF-p1C; SEQ ID NO: 1) ; and

d) KIRALKWKNAHLKQEIAALEQEIAALEQ (SAF-p2C; SEQ ID NO: 5).

16. (Original) A protein structure according to anyone of claims 1 to 14 or a peptide monomer unit according to claim 15 wherein at least one amino acid residue is derivatised.

17. (Original) A branching self-assembling fibre comprising two or more protein structures according to anyone of claims 1 to 11, coupled together to form a T-shaped conjugated structure.

18. (Original) The branching self-assembling fibre of claim 17, wherein at least one of the protein structures comprises one or more central cysteine residues, and at least one other protein structure comprises a terminal cysteine residue.

19. (Original) A method of producing protein structures, the method comprising providing a mixture of first and second monomer units which associate to form a protein structure according to any one of claims 1 to 14, wherein the first and second monomer units comprise the heptad repeat motif (abcdefg) and/or the hendecad repeat motif (abcdefghijk).

20. (Original) A method according to claim 19 in which the protein structure is derivatised.

21. (Original) A method according to claim 19 or 20 in which the protein structure is stabilised by cross-linking.

22. (Original) A protein fibre produced by an association of protein structures according to any one of claims 1 to 14.

23. (Original) A kit for making a protein structure, the kit comprising first and second peptide monomer units which associate to form a protein structure according to any one of claims 1 to 14 or a protein fibre according to claim 22, wherein the first and second monomer units comprise the heptad repeat motif (abcdefg) and/or the hendecad repeat motif (abcdefghijk).

24. (Original) A two dimensional grid comprising a protein structure according to any one of claims 1 to 14 or a protein fibre according to claim 22.

25. (Original) A three dimensional matrix comprising a protein structure according to any one of claims 1 to 14 or a protein fibre according to claim 22.

26. (Original) A matrix according to claim 25 which is managed to assemble in solution.

27. (Original) A matrix according to claim 25 or claim 26, wherein one or more binders is fused to the protein structure, wherein the one or more binders are aligned to give high avidities for one or more target entities.

28. (Original) A matrix according to anyone of claims 2S to 27 which is arranged to bind one

or more target entities.

29. (Original) A matrix according to claim 28 which is arranged to bind viruses.

30. (Original) A method of forming a matrix according to anyone of claims 25 to 29 in which a mixture of separate first and second monomer units is provided, wherein the first and second monomer units comprise the heptad repeat motif (abcdefg) and/or the hendecad repeat motif (abcdefghijk) and are caused to associate to form a plurality of protein structures according to anyone of claims 1 to 14, wherein the protein structures assemble to form a three-dimensional matrix.

31. (Original) A method according to claim 30 in which the matrix is formed *in situ*.

32. (Original) A method for controlling the production of a synthetic polymers comprising assembling a protein structure in accordance to any one of claims 1 to 14 in association with the polymer.

33. (Original) A method according to claim 32 in which the protein structure is removed after synthesis of the polymer.

34. (Original) A tip for use in Atomic Force Microscopy comprising a protein structure according to anyone of claims 1 to 14.